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About: Results were produced by the GenCore software, version 4.5,.
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Date: Sep 23, 2001 12:04 PM

Command line parameters:
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-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000000
-USER=US08978217_@CGN1_1_85 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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Search Information block:
Query: US-08-978-217-2
Query length: 371
Database: Issued_Patents_NA:*
Database sequences: 324599
Database length: 94655562
Search time (sec): 115.040000

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; Sequence 1, Application US/0874678904
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tymms, Christine DeBouck
; TITLE OF INVENTION: A No. 5789200e1 Human ETS Family Member, ELF3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: NO. 5789200ember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-08-746-789A-1

alignment_scores:
Quality: 1980.00
Ratio: 5.337
Percent Similarity: 100.000   Percent Identity: 100.000

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Length: 371
Gaps: 0

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~ seq_documentation_block:
~ Sequence 2, Application US/09009913
~ Patent NO. 6087485
~ GENERAL INFORMATION:
~ APPLICANT: Axys Pharmaceuticals, Inc.
~ TITLE OF INVENTION: Asthma Related Genes
~ NUMBER OF SEQUENCES: 339
~ CORRESPONDENCE ADDRESS:
~ ADDRESSEE: Bozicevic & Reed, LLP
~ STREET: 285 Hamilton Ave, Suite 200
~ CITY: Palo Alto
~ STATE: CA
~ COUNTRY: USA
~ ZIP: 94301
~ COMPUTER READABLE FORM:
~ MEDIUM TYPE: Diskette
~ COMPUTER: IBM Compatible
~ OPERATING SYSTEM: DOS
~ SOFTWARE: FastSEQ for Windows Version 2.0
~ CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/09/009,913
~ FILING DATE: 21-JAN-1998
~ CLASSIFICATION:
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER:
~ FILING DATE:
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Sherwood, Pamela J
~ REGISTRATION NUMBER: 36,677
~ REFERENCE/DOCKET NUMBER: SEQ-4P
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: 650-327-3231
~ TELEFAX: 650-327-3231
~ TELEX:
~ INFORMATION FOR SEQ ID NO: 2:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 5427 base pairs
~ TYPE: nucleic acid
~ STRANDEDNESS: double
~ TOPOLOGY: linear
~ MOLECULE TYPE: cDNA
~ US-09-009-913-2

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US-08-978-217-2 x US-09-009-913-2

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1215 CCAGAGTCGGAAC 1227
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84 GCTGCCTCCCCTCCATCAGCCACAGCTATTGGATTTCCCACCCAGAATCT 133

40 uValLeuThrLeuSerAsnProGlnMetSerLeuGluGly.......... 53
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134 TTAGGTA........AATGAGATCATGATTCTTGGAAGGAGGAGGTGGTGTAA 174

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 67 pSerLysThrGlnValLeuAspTrpIleSerThrTyrGlnValGlyLysAsnL  84
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315 GTCGAAGACGCAGGTTCTGGACTGGATCAGCTACCAACTGGGAAGAAACA 364

 84 ystTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
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365 AGTACGACGCAAGCGCCATTGACTTCTCACGATGTGACATGGATGGGGGCC 414

101 ThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProIle 117
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415 ACCCTCTGCAATTGTGCCCTTGAGGAGCTGCGTTCTGGTTCTTTGGGCCTCT 464

117 uGlyAspGlnLeuHisAlaGlnIleLeuArgAspLeuThrSerSerSerA 134
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465 GGGGGACCAAACTCCATGCCCAGCTGCCAGACCTTCACTTCCAGCTTCTG 514

134 spGluLeuSerTrpIleIleLeuGluLeuLeuLysAspGlyMetAlaPhe 150
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515 ATGAGCTCAGTTGGATCATTGAACGTGCTGGAGAAGGAATGGCCTTC 564

151 GlnGluAlaLeuAspProGlyTyrProPheAspGlnGlySerProPheAlaGl 167
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565 CAGGAGGCCCTAGACCCAGGGCCCTTGACCAGGGCAGCCCCCTTTGCCCA 614

167 nGluLeuLeuAspAspAspProGlyGlnGlnAlaSerProTyrHisProGlySerC 184
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615 GGAGCTCCTGGACGACGGTCAGCAAGCCAGCCCCTACCACCCCGGCAGCT 664

184 ysGlyAlaGlyValAlaProSerProGlySerSerAspValSerThrAlaGly 200
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665 GTGGGCGCAGGAGCCCCTCCCGGCCAGCTCTGACGTCTTCCACCGCAGG 714

201 ThrGlyAlaSerArgSerHisSerSerAspSerGlyGlySerAspVa 217
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217 lAspLeuAspProThrAspPheGlyGlnIleSerLeuPheProSerAspGlyPheArga 234
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765 GGACCTGGATCCCACTGACTTCGGCCAGATCTCTCCAGCCGATGGGTTTCGTG 814

234 spCysLysLysGlyAspProLysProLysGlySerHisSerGlyLeuTyrArgPro 250
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251 ArgLysLeuSerLysGluTyrTrpTrpAspAspCysLeuGlyLysLysSerGly 267
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267 sHisSerAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeur 284
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284 leHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGlu 300
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 59 pLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpI              76
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275 GCAATGAAATTCATCCTCAGTACTGGACCAAGTACCAGGTGTGGGAGTGGC             324
 76 leSerTyrGlnValGlyLysAsnLysTyrTyrAlaSerAlaIleAlaSpPhe           92
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325 TCCAGCACCTCCTGGACACCAACCAGCTGGATGCCAATTGTATCCCTTTC             374
 93 SerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGluGlu          109
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375 CAAGAGTTCGACATCAACGGCGAGCCACTTCTGCAGCCATGAGTTTGCAGGA          424
109 uLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuA            126
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425 GTTCACCCGGGGCGGCAGGGACGGCGGGGGAGCTCCTCTACAGCAACTTGC           474
126 rgAspLeuThr........SerSerSerSerAspGluLeuSerTriPle            139
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475 AGCATCTGAAGTGGAACGGCCAGTGCAGTAGTGAC                          509
140 IleGluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspPr           156
510 ........................CTGTTCCAGTCC.............            521
156 oGlyProPheAspGlnGlySerProPheAlaGlnGlnGluLeuLeuAspAspG        173
522 ........................ACACACAAATGTCATTGTCAAGA             543
173 lyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGlyAlaPro          189
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544 CTGAACAAACTGACCT                                           560
190 SerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSe          206
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238 ............GlyAspProLysHisGlyLy                          244
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244 sArgLysArgGlyArgProArgLysLeuSerGluTyrTrpAspCysL          261
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713 AAAGGAGCAAAGAGACCCCCTGCCAAGTGCCACACCAAA                  749
261 euGluGlyLysLysSerHisAlaProArgGlyThrHisLeuTrpGlu          277
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294 sTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAlaV       311
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833 ATGGGAAGAAGAGACCGATCTGAGGGCGTCTTCAGGTTCTTGAAATCAGAGGG   882
311 aIaLaGlnLeuTrpLysGlyGlnLnLeuLysLysSerAsnSerAsnMetThrTyrGlu 327
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344 gValAspGlyArgArgLeuValTyrLysPheGlyLysSerSerGlyTyr         361
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1033 GGAGAGAAAATGAA                                           1046
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seq_documentation_block:
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; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axys Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5510 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-913-3

alignment_scores:
Quality: 555.50   Length: 322
Ratio: 2.939   Gaps: 8
Percent Similarity: 58.696   Percent Identity: 39.130

alignment_block:
US-08-978-217-2 x US-09-009-913-3

Align seq 1/1   to: US-09-009-913-3   from: 1   to: 5510   ..

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 59 TrpLeuGlyGlnProGlnPheTrpSerLysThrGlnValLeuAspTr    75
    ||| :::|||||||:::||||||:::||||:||||||||||||:||
356 TGGCATGAAATTCATCCTCAGTACTGGACCAAGTACCAGGTGTGGGAGTG  405
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seq_name: /cgn2_6/ptodata/2/1na/6a_COMB.seq:US-09-009-913-4
documentation_block:
; Sequence 4, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
;   APPLICANT: Axys Pharmaceuticals, Inc.
;   TITLE OF INVENTION: Asthma Related Genes
;   NUMBER OF SEQUENCES: 339
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Bozicevic & Reed, LLP
;     STREET: 285 Hamilton Ave, Suite 200
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/009,913
;     FILING DATE: 21-JAN-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Sherwood, Pamela J
;     REGISTRATION NUMBER: 36,677
;     REFERENCE/DOCKET NUMBER: SEQ-4P
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-327-3231
;     TELEFAX: 650-327-3231
;     TELEX:
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5667 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-009-913-4

alignment_block:
US-08-978-217-2 x US-09-009-913-4

alignment_scores:
          Quality:   555.50           Length:      322
            Ratio:     2.939             Gaps:        8
Percent Similarity:  58.696   Percent Identity:  39.130

Align seg 1/1   to: US-09-009-913-4   from: 1   to: 5667
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;  APPLICANT: Axys Pharmaceuticals, Inc.
;  GENERAL INFORMATION:
;  Patent No. 6087485
;  Sequence 338, Application US/0909913
seq_documentation_block:
seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-009-913-338
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```
;  TITLE OF INVENTION: Asthma Related Genes
;  NUMBER OF SEQUENCES: 339
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Bozicevic & Reed, LLP
;    STREET: 285 Hamilton Ave, Suite 200
;    CITY: Palo Alto
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94301
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/009,913
;    FILING DATE: 21-JAN-1998
;    CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:
;    FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Sherwood, Pamela J
;    REGISTRATION NUMBER: 36,677
;    REFERENCE/DOCKET NUMBER: SEQ-4P
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 650-327-3231
;    TELEFAX: 650-327-3231
;    TELEX:
;  INFORMATION FOR SEQ ID NO: 338:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 848 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;    MOLECULE TYPE: cDNA
;    FEATURE:
;      NAME/KEY: Coding Sequence
;      LOCATION: 1..848
;      OTHER INFORMATION:
US-09-009-913-338
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alignment_scores:
  Quality:              486.50        Length:             295
  Ratio:                2.764         Gaps:                 5
  Percent Similarity:   59.661        Percent Identity:  36.949

alignment_block:
US-08-978-217-2 x US-09-009-913-338

Align seq 1/1   to: US-09-009-913-338    from: 1 to: 848
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 57 AlaSerTrpLeuGlyGlnInProGlnPheTrpSerLysThrGlnInValIle  73
    |:::||||        |||||:::||||:::|||:::||
118 AGCCAGTGGCATGAAATCCACCCTCAGTACTGGACCAAAATACCAGGTGTG 167

 73 uAspTrpIleSerTrpGlnValGlyLysAsnLysTyrTyrAspAlaSerAlaIal  90
    :::|||:::|||       :::||||||:::|||||:::|||||:::||
168 GGAATGGCTGCAGCACCTCCTGGACACCAACCAGCTAGACGCTAGCTGCA 217

 90 leAspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCyssAla 106
    ||        |||||:::|||::::|||||||||:::|||:::
218 TCCCTTTCCAGGAGTTCGACATTAGCGGAGAACACCTGTCGCAGCATGAGT 267

107 LeuGluGluLeuArgLeuValPheGlyProLeuGlyAspProLeuHisIal 123
    |:::     |||:||:::       |||:||||||:::|||:::
268 CTGCAGGAGTTCACGAGGCGAGCAGGCCTCAGCTGGGCAGCTCTCACAG 317

123 aGlnLeuArgAspLeuThr.........SerSerSerAspLeuSerAspLeuSer... 137
    :::|||:|||:::        |||         |||||||||  :::
318 CAACCTACAGCACATCTCAAGTAGGACGGCCAATGCAGCAGTTGACCTTTTCC 367
```

```
663 GAGTTCACCCGCGGGGCGCAGGAGGACGGGCGCGGGGCAGCTCCTTCCTACAGCAACTT 712
125 uArgAspLeuThr..........SerSerSerSerAspGluLeuSerTrpI 139
    |:::  |||                |||||||||||||
713 GCAGCACTGGAAGTGGAACGGCCCAGTGCAGTACTGAC.............. 749
139 leIleGluLeuLeuGlyLysAspGlyMetAlaPheGlnGluAlaLeuAsp 155
    |||||||:::
750 .................CTGTTCCAGTCC............ 761
156 ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAs 172
762 ...................ACACACAAATGTCATTGTGTCAA 781
172 pGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGlyAlaP 189
    :::||||||:::::::::
782 GACTGAACAAACTGAGCCT............ 800
189 roSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArg 205
    :::||||
801 ........................TCCATCATGACAACACCTGGAAAGACGAG 827
206 SerSerHisSerSerAspSerGlyGlySerAspValAspLeuAspProTh 222
    |||:|||         |||||||||
828 AACTATTTATATGACACCAACTATGGTAGCACAGTAGGATTTG........TT 871
222 rAspGlyGlyLysLeuPheProSerAspGlyPheArgAspCysLysLys... 237
    |||:::
872 GGACAGCAAAAACTTTC........ TGCCGGGCTCAGA 900
238 .....................GlyAspProLysHisGly 243
    :::||||
901 TCTCCATGACAACCACCAGTCACCTTCCTGTTGCAGAGTCACCTGATATG 950
244 LysArgLysArgGlyArgProArgLysLeuSerGluTyrTrpAspPCy 260
    |||:::
951 AAAAAGGAGCAAGAACCCCCCTGCCAATTGCCACCACCAAA.... 989
260 sLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpC 277
    |||||||||
990 ....................AAGCACAACCGAGAGGGACTCACTTATGG 1020
277 luPheIleArgAspIleLeuHisProGluLeuAsnGluGlyLeuMet 293
    |||||||||||        ||  |||:::
1021 AATTCATCCGCGACACTCCTTGAACCCAGACAAGAGAACCCAGGATTAATA 1070
294 LysTrpGluAsnArgHisGlyValPheLysPheLysArgSerGluLVaI 310
    |||:::||||        |||||:::||||:::|||:::||
1071 AAAATGGGAAGAACCGGATCTGAGGGCCGTCTTCAGGTTCTTGAAATCAGAGGC 1120
310 aValAlaGlnLeuTrpTrpGlyGlnLysLysLysAsnSerAsnMetThrTyrG 327
    :::|||:::|||       |||||||:::|||||||:::||||:::||
1121 AGTGGGCTCAGCTATGGGGTAAAAAAGAAGAACAACAGCAGCATGACCTATG 1170
327 luLysLeuSerArgAlaMetArgTyrTyrTyrTyrTyrLysSerArgGluIleLeuGlu 343
    |||||||||||:::         |||:||:::|||||||||:::
1171 AAAAGCTCAGCCGAGCTATGAGATATTACTACAAAAGAGAAATACTGGAG 1220
344 ArgValAspGlyArgArgLeuValThrTyrLysPheGlyLysSerAsnSerSerG1 360
    ||||||:::|||||||||||||||:::||||||:::|||:::
1221 CGTGTGGATGGACGAAGACTGGTTATATAAATTTGGGAAGAGAAATCCCGAGG 1270
360 yTrpLysGlyGluGlu 365
    ||||||:::||
1271 ATGGAGAGAAAATGAA 1286
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seq_documentation_block:
Sequence 8, Application US/0909913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: Axys Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-009-913-8

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-009-913-8

alignment_scores:
Quality: 422.00
Ratio: 2.605
Percent Similarity: 52.597   Percent Identity: 29.221

alignment_block:
US-08-978-217-2 x US-09-009-913-8

Align seq 1/1 to: US-09-009-913-8 from: 1 to: 2280

Length: 308
Gaps: 5

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seq_documentation_block:
  Sequence 6, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
;   APPLICANT:
;     APPLICANT:  Axys Pharmaceuticals, Inc.
;   TITLE OF INVENTION:  Asthma Related Genes
;   NUMBER OF SEQUENCES:  339
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Bozicevic & Reed, LLP
;     STREET:  285 Hamilton Ave, Suite 200
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94301
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09,009,913
;     FILING DATE:  21-JAN-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Sherwood, Pamela J
;     REGISTRATION NUMBER:  36,677
;     REFERENCE/DOCKET NUMBER:  SEQ-4P
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650-327-3231
;     TELEFAX:  650-327-3231
;     TELEX:
; INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2428 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
; US-09-009-913-6
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-009-913-6

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alignment_scores:
          Quality:  422.00            Length:  308
            Ratio:  2.605               Gaps:  5
Percent Similarity:  52.597  Percent Identity:  29.221

alignment_block:
  US-08-978-217-2 x US-09-009-913-6

Align seq 1/1   to: US-09-009-913-6   from: 1   to: 2428
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 59 TrpLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTr  75
    |||  :::  ||||||||||:||||||  ::::|::||  |||| ::||
354 TGGACATCAGTCCACCCTGAATACTGGACTAAGGCCCATGTGTGGGAGTG 403

 75 pIleSerTyrGlnValGlyLysAsnLysTyrAspAlaSerAlaIleAspP  92
    |::::::::::  |||  |||||||::::::|:||:::|  |:::|
404 GCTCCAGTTCTGCCTGGGACCAGTACAAGTTGGACACCAATTGCCATCTCCT 453

 92 heSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGlu 108
    :::::|||::::  |||:::|:|||||:  ::::::|||:::|||:::
454 TCTGCAACTTCAACATCAGTTGGCCTGCAGCGTGCACGCATGACACAGGAG 503

109 GluLeuArgLeuValPheGlyProLeuGlyLysAspGlnLeuHisAlaGlnLe 125
    |||:::  |||:::  |||  |||:::  ||||  :::|||  |||:::
504 GAGTTCGTCGAGGCAGGCTGGGCCTCGCGGCGGAGTACCTGTACTTCAATCCT 553

125 uArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrpIleIleGluL 142
    :::::::::  :::
554 CCAGAACATCCGCACA.                                    569

142 euLeuGluLysAspGlyMetAlaPheGlnGlnValAlaLeuAspProGlyPro 158
    ::::::::::                                            569
...

158 SerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLy 175
570 ...CAAGGTTACTCCTTTTTTTAATGACGCTGAGAGAAAGCAAGGCCAC 613

175 nAlaSerProTyrHisProGlySerCysGlyAlaGlyIleAlaProSerProG 192
    :::  :::  |||::::::::|||
614 CATCAAAGACTATGCTGATTCCAACTGC.                        641

192 lySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHis 208
    :::::::::||||:::::||||                               
642 ...TTGAAAACAAGTGGCATC. AAAAGTCAAGACTGTCAC           677

209 SerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLy 225
678 AGT.                                                 680

225 sLeuPheProSerAspGlyPheArgAspCysLysGlyAspProLysH 242
680 ........                                             680

242 1sGlyLysArgGlyAsrGlyArgProArgLysLeuSerLysGluTyrTrp 258
680 ........                                             680

259 AspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisIle 275
    |||:::|||:::|:::::::::|:::::||::::|:::|||:::|||||||
681 ...CATAGTAGAACAACAAGCCTCCAAAGTTCTCATCT               712
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530 AGT.                                                 532
225 sLeuPheProSerAspGlyPheArgAspCysLysGlyAspProLysH    242
532 ........                                             532
242 1sGlyLysArgGlyAsrGlyArgProArgLysLeuSerLysGluTyrTrp  258
532 ........                                             532
259 AspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisIle 275
    |||:::  :::                  :::::::::||||
532 ........                                             532
533 ...CATAGTAGAACAAGCCTCCAAAGTTCTCATCT                 564
275 uTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyL  292
    |||||||::::  ||:::||||||||||:::  |||  |||  :::||
565 ATGGGAAATTTGTACGAGACGACCTCGTTCTATCTCCTGAAGAAAACTGTGGCA 614
292 euMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSer  308
    ::||:||||:::||||||||:::||:::  ||||:::::::::||||
615 TTCTGGAATGGGAAGAGAGATAGGGAACAAGGAAATTTTCGGGTGGTTAAATCG 664
309 GluAlaValAlaGlnLeuTrpProGlyGlnLysLysLysAsnSerAsnMetTh 325
    ||||||:::  ||:::||||||:::||||||||||  :::::||||||
665 GAAGCCCTGGCAAAGATGTGGGGACAAAGGAAGAAAAATGACACAGAATGAC  714
325 rTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrTyrLysArgGluIleT 342
    |:::||||||:::  |||||||||:::  ||||||||||||||:::
715 GTATGAAAAGTTGAGCAGAGCCCTGAGATACTACTATTATAAAACAGGAATTT 764
342 euGluArgValAspGlyArgArgLeuValThrTyrTyrLysPheGlyLysAsnSer 358
    :::||||||:::|||||||||||||||:::  ||||||  |||:::|||
765 TGGAGCAGCGGTTGAC...CGAAGGTTAGTGTACAAAATTTGGAAAAAATGCA  811
359 SerGlyThrTrpLysGlyGluGluValVal                      366
    ||||:::  |||:::
812 CACGGGTGGCAGGAGAACAAGCTA                             835
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Left column

alignment_scores:
Quality: 422.00   Length: 308
Ratio: 2.605   Gaps: 5

US-09-009-913-10
MOLECULE TYPE: cDNA
TOPOLOGY: linear
STRANDEDNESS: double
TYPE: nucleic acid
LENGTH: 2498 base pairs
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 10:

TELEX:
TELEFAX: 650-327-3231
TELEPHONE: 650-327-3231
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: SEQ-4P
REGISTRATION NUMBER: 36,677
NAME: Sherwood, Pamela J
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
CLASSIFICATION:
FILING DATE: 21-JAN-1998
APPLICATION NUMBER: US/09/009,913
CURRENT APPLICATION DATA:
SOFTWARE: FastSEQ for Windows Version 2.0
OPERATING SYSTEM: DOS
COMPUTER: IBM Compatible
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
ZIP: 94301
COUNTRY: USA
STATE: CA
CITY: Palo Alto
STREET: 285 Hamilton Ave, Suite 200
ADDRESSEE: Bozicevic & Reed, LLP
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 339
TITLE OF INVENTION: Asthma Related Genes
APPLICANT: Axys Pharmaceuticals, Inc.
GENERAL INFORMATION:
Patent No. 6087485
Sequence 10, Application US/09009913
seq_documentation_block:

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:us-09-009-913-10

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275 uTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyL 292
    ||||||||||||:::|||||||      |||||      |||
713 ATGGGAATTTGTACGAGAGACCTGCTTCTATCTCCTGAAGAAAACTGTGCCA 762

292 euMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSer 308
    :::||||||||||||:::||||||||:::||||::||||||::|||
763 TTCTGGAATGGGAAGATAGGGAACAAGGAAATTTTTCGGCTGGTTAAATCG 812

309 GluAlaValAlaLeuGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetH 325
    ||||:|||||||||||||||:||||||||||:::
813 GAAGCCCTGGCAAAGATGTGGGGACAAAAGGAAGAAAAATGACAGAATGAC 862

325 rTyrGluLysLeuSerArgArgAlaMetArgTyrTyrTyrTyrLysArgGluIleL 342
    |||||||||||||||||||||||:::||||||||||     |||
863 GTATGAAAAGTTGAGCAGACGCCCTGAGATATCACTTACTATAAAAACAGGAATGAC 912

342 euGluArgValAspGlyArgArgLeuValTyrTyrTyrTyrLysArgGluIleL 358
    |||||||||||||||||||||||||||||||||||
913 TGGAGCGGGTTGAC...CGAAGGTTAGTTGTACAAATTTGGAAAAAATGCA 959

359 SerGlyTrpLysGluGluGluVal 366
    |||||||||
960 CACGGGTGGCAGGAAGACAAAGCTA 983
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Right column

Percent Similarity: 52.597   Percent Identity: 29.221

alignment_block:
US-08-978-217-2 x US-09-009-913-10

Align seq 1/1   to: US-09-009-913-10   from: 1   to: 2498

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 59 TrpLeuGlyGlnProGlnPheTrpSerLysThrGlnValLeuAspTr 75
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423 TGGACATCAGTCACCACCCTGAATACTGGACTAACGCCCATGTGTGGGAGTG 472

 75 pIleSerThrTyrGlnValGluLysLeuAsnLysTyrAspSerAlaIleAspP 92.
    |||:::      |||:::      |||      |||||      |||:::      |—|
473 GCTCCAGTTCTGCTGCCGACCAGTACAAGTTGGACACCAACAAACTGCACTCCT 522

 92 heSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGlu 108
    :::      |||      |||      |||:::      |||      |||:::
523 TCTGCAACTTCAACATCAGTGGCCTGCAGCTACAGGTTGCAGCATGACACAGGAG 572

109 GluLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnIle 125
    |||:::      |||      ||:::      |||:::      |—|
573 GAGTTCGTCGAGGAGCTGGCCCTTGCGGGGAGTACCCTGTACTTCCATCCT 622

125 uArgAspLeuThrSerSerSerSerAspGlyLeuSerTrpIleIleGluL 142
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623 CCAGAACATCCGACA 638

142 euLeuGlyLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro 158
    |||:::      |||||      |||
711 TTGAAAAACAAGTGGCATC...AAAAGTCAAGAGACTGTCAC 746

159 PheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGl 175
    |||||      :::|||
639 ...CAAGGTTACTTCCTTTTTTAATGACGCTGAAGAAAGCAAGGCCAC 682

175 nAlaSerProTyrHisProGlySerCysGlyAlaGlyValAlaProSerPro 192
    :::|||||      :::|||||      |||
523 CATCAAAAGACTATGCTGATTCCAACTGC... 710

192 lySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHis 208
    :::|||:::|||||      |||||
711 TTGAAAAACAAGTGGCATC...AAAAGTCAAGAGACTGTCAC 746

209 SerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLy 225
    |||||||
639 ...CAAGGTTACTTCCTTTTTTAATGACGCTGAAGAAAGCAAGGCCAC 682

225 sLeuPheProSerArgSerGlyPheArgAspCysLysLysGlyAspProLysH 242
    |||
747 AGT... 749

242 isGlyLysArgGlyArgProArgLysLeuSerGlyGluTyrTrp 258
    |||
749 ... 749

259 AspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisIle 275
    |||:::||||||
782 CATAGTAGAAACAAGGCCTTCCAAAGTTCTCATCT 831

275 uTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyL 292
    ||||||||||||:::|||||||      |||||      |||
782 ATGGGAATTTGTACGAGAGACCTGCTTCTATCTCCTGAAGAAAACTGTGCCA 831

292 euMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSer 308
    :::||||||||||||:::||||||||:::||||::||||||::|||
832 TTCTGGAATGGGAAGATAGGGAACAAGGAAATTTTTCGGCTGGTTAAATCG 881

309 GluAlaValAlaLeuGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetH 325
    ||||:|||||||||||||||:||||||||||:::
882 GAAGCCCTGGCAAAGATGTGGGGACAAAAGGAAGAAAAATGACAGAATGAC 931

325 rTyrGluLysLeuSerArgArgAlaMetArgTyrTyrTyrTyrLysArgGluIleL 342
    ||||||||||||||||||||||
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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-368-281-1

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 932 GTATGAAAAGTTGAGCAGAGCCCTGAGATACTACTATAAACAGGAATTT 981
     ||||||||||||||||||||||||||:||||||
 982 TGGAGCGGGTTGAC...CGAAGGTTAGTTGTACAAAATTTGGAAAAAATCA 1028
```

```
 342 euGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
     ||||||||||||||:|||||
 982 TGGAGCGGGTTGAC...CGAAGGTTAGTTGTACAAAATTTGGAAAAAATCA 1028
```

```
 359 SerGlyTyrTrpLysGluGluGluVal 366
     ||||||||||:||||||:|||||
1029 CACGGCGTGGCAGGAAGAGACAAGCTA 1052
```

Patent No. 5721113, Application US/08368281

alignment_block:
US-08-978-217-2 x US-08-368-281-1

Align seq 1/1 to: US-08-368-281-1 from: 1 to: 2975

alignment_scores:
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           Ratio:   1.773          Gaps:   10
Percent Similarity: 49.291   Percent Identity: 26.241
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 139 IleIleGluLeuGluGlyLysAspGlyMetAlaPheGlnGlyAlaLeuAs 155
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   1 GTGGTGAGTGTGTTGTCGGTCGCACGGCGGTGGTGTCCGGCGGGGGGTCC 50
```

```
 155 pProGlyProPheAspGlnGlySerProPheAlaLeuGlnGluLeuLeuAspA 172
     |||:|||||||:||||||||::::|||
  51 GCCTCTCCCCTG...........CCGCCCGCTGCTCACGGTGGTGAAGTCAATG 91
```

```
 172 spGlyGlnGlnAlaSerPro.................. 178
     ||||||                     :::|||
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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-368-281-3

```
  92 TGAACGAGCAGCTCCAGCCCCGGGATAAACATGGGGACGGGGACGTCTCTGCCATGA 141
     ||||||||||||||:||||
 179 .........TyrHisProGlySerCysGlyLysAlaGlyAlaProSerProGlySe 193
```

```
 142 GGGACCACCAGAACCA.........GCTGGATCTGCTCATCCGGCCCG 179
     ||||||||:||            ||||||
 179 .........TyrHisProGlySerCysGlyLysAlaGlyAlaProSerProGlySe 193
```

```
 193 rSerAspValSerThr.................. 198
     ::|||||||:|||:||
 180 TGGAAGCATCAGTTCACGACGCAGTAATGCACACTGTACAGATAAGACAATT 229
```

```
 199 .........AlaGlyThrGlyAlaSer............ 204
     ||:::|||       |||
 230 GAAGCTGCTGAAGCCCTGCTTCATATGGAAATCCTCCTACCTGCTTGAGGGA 279
```

```
 205 ..................ArgSerSerHi 208
     :::||
 280 TTCAAGAAGTGTCCTGAATTCATCCATGCTGCTATGAGGCCAGAATGTCATTA 329
```

```
 208 sSerSerAspSerGlyGly.SerAspValAspLeuAspProThrAspGly 224
     ||||||||||| |||   |||      |||
 330 CAGAAACTGTAGTGGAGGTGTCAACTGAAGAGTCTGAAGCCCATGGATACC 379
```

```
 225 LysLeuPheProSer.........AspGlyPheArgAspCysLysLysLys...... 237
     |||:||   :|||   ||||||
 380 TCTCCTATTCCAAATCACCACAGATACCAGCCATGCAACCAAATGAAAAAGAAAAA 429
```

```
 238 ....................GlyAspP 240
     ||:|||
 430 AGTTGGCCGTAAACCAAAGACCCACCAGCAAATCACCAACAATTTCCAATGGGTCTC 479
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```
 240 rolysHisGlyLysArgGlyArgGlyArgProArgLysLeuSerLysGlu 256
     |||:||  ||||:|||:|||      |||
 480 CTGAGTTAGGTTATAAAGATAAGAAAACCAAGA 508
```

```
 257 TyrTrpAspCysLeuGlyGlyLysLysSerLysHisAlaProArgGlyTh 273
     |||||||||
 509 ..........GAAGAAAAGGAAACACA 528
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```
 273 rHisLeuTrpGluPheIleArgAspIleLeuHisProGluLeuAsnG 290
     |:::||||:|||||     :||
 529 CTATTTGTGGGAGTTCTTTTAGATCTACTTCAAGATAAAAATACTTGTC 578
```

```
 290 luGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeu 306
     ::|||||   |||:|||||||||:||||||:||:::
 579 CCAGGTATATTAAATGGACTCAGAGACAAAAAGGCATATATTCAAGCTGGTG 628
```

```
 307 ArgSerGluAlaLaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAs 323
     |||:||||||||||||||||||||||||||||||
 629 GATTCAAAAGCCTGTCTTCTTAAGCTTTGGGGAAAGCATTAAGAACAAACCAGA 678
```

```
 323 nMetThrTyrGluLysSerArgAlaMetArgTyrTyrTyrTyrLysArgG 340
     ||||:::|||||||
 679 CATGAACTATGAAAACCATGGGACGAGCTTTGAGATACTACTACCAAAGGG 728
```

```
 340 luIleLeuGluArgValAspGlyArgArgLeuValTyrLysPhe 354
     ||||||   :::||||||:|||   ::||||||||:|||:||
 729 GAATTCTTGCAAAGGTTGAAGGACAGAGGCTTGTATATCAGTTC 772
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;       STATE: Pennsylvania
;       COUNTRY: USA
;       ZIP: 19406
;  COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/368,281
;       FILING DATE:
;       CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;       NAME: Baumeister, Kirk
;       REGISTRATION NUMBER: 33,833
;  TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 610-270-5096
;       TELEFAX: 610-270-5090
;  INFORMATION FOR SEQ ID NO: 3:
;  SEQUENCE CHARACTERISTICS:
;       LENGTH: 3240 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
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US-08-368-281-3

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Percent Similarity: 54.872    Percent Identity: 32.308
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alignment_block:
US-08-978-217-2 x US-08-368-281-3

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190 SerProGlySerSerAspValSerThrAlaGlyThrGly..........      202
506 AGCCCTGCTTCATATGGAATCTCCTACCTGCTTGAGGGATTCAAGAAGTC     555

203 ...........AlaSerArgSerSerHisSerSerAspS               212
556 CTGAATTCATCCATGCTGCTATGAGGCCAGATGTCATTACAGAAACTGTA     605

212 erGlyGly.SerAspValAspLeuAspProThrAspGlyLysLeuPhePr    228
606 GTGGAGGTGTCAACTGAAGAGTTCTGAACCCATGGATACCTCTCCTATTCC    655

228 oSer........AspGlyPheArgAspCysLysLys..........        237
656 AACATCACCAGATAGCCATGAACCAATGAAAAAAGAAAAAGTTGGGCCGTA    705

238 ...........GlyAspProLysHisGly                         243
706 AACCAAAGACCCAGACAATCACCAAATTCCAATGGGTCTCCTGAGTTAGGT    755

244 LysArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCy    260
756 ATAAAGAAGAGAAAACCAAGA                                 773

260 sLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpG    277
774 ....GAAGGAAAAGGAAACACA..........ACCTATTTGTGG         -804

277 luPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMet    293
805 AGTTTCTTTTAGATCTACTTCAAGATAAAAATAACTTGTCCCAGGTATATT    854

294 LysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAl    310
855 AAAATGGACTCAGAGAGAAAAAAGGCATATTTCAAGCTGGTGGATTCAAAGGC  904
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seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-360-779-1-

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310 avalaLaGlnLeuTrpGlyLysGlnLysLysLysAsnSerAsnMetThrTyrG   327
905 TGTCTCTAAGgCTTTTGGGGAAAAGCATAAGAACAAAACCAGAACATGAACATG   954

327 luLysLeuSerArgAlaMetArgTyrTyrTyrLysArgSerArgGluIleLeuGlu 343
955 AAACCATGGGACGAGACCTTTGAGATAACTACTACCAAAGGGAATTCTTGCA   1004

344 ArgValAspGlyArgArgLeuValTyrLysPhe                    354
1005 AAGGTGAAGGACGAGAGGCTTGTATATACAGTTC                  1037
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alignment_block:
US-08-978-217-2 x US-09-360-779-1

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116 ProLeuGlyAspGlnLeuHisAla..........GlnLeuArgAspLe    128
133 CCTCTGGGGGGAGAGGGTTCCAGCCCCCACCCCCTCAGCCCCATCCCCT    182

128 uThr.......SerSerSerSerAspSerTrpIleIleGluGluLeuL    143
183 CACAGCTCACTCTCCCAGTACACCGGCACCGGGATGGGCCT           222

143 euGluLysAspGlyMetAlaPheGlnLeuAlaLeuAspProGlyProPhe  159
223 ...........GGGATGCAGCTCCAGGACCCCCTCCCTCCT...CACCAC   258

160 AspGlnGlySerProPheAlaGlnLeuLeuLeuAspProGlyGlnIleAl  176
259 ACCCTGGCTGCCCGCCTCCCCGCCAGGCCTTGCCCGGACCCCGGCGGGCTCTAC 308

176 aSerProTyrHisProGlySerCysGlyValAlaGlyAlaProSerProGlyS  193
309 TCTTCCCGTGTCACCCACACAGTCACCACGCGGCGGGGTATCGGCGCCACCCCAAGCG 358

193 erSer.........AspValSerThrAlaGlyThrGlyAlaSerArg      205
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alignment_block:
US-08-978-217-2 x US-09-344-579-1

alignment_scores:
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Percent Similarity:  52.349         Percent Identity: 22.595
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seq_documentation_block:
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Sequence 1, Application US/0934457
Patent No. 6054316
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
FILE REFERENCE: RTS-0063
CURRENT APPLICATION NUMBER: US/09/344,579
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (291)..(1700)
US-09-344-579-1
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:us-09-344-579-1

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241 LysHisGlyLysArgGlyAlaArgProArgLysLeuSerLysGluTy 257
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1251 TCTCTCTGCCTCAATAAGCCAACCAATGTCTTCAAGGATTA 1291

257 rTrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGly.... 272
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1292 CATCCAA.........GAGAGGAGTGACCCAGTGAGCAAGGCAAAC 1329

273 .........................................Thr 273

1330 CAGTTATACCTGCCAGCTGTGCTGCCCGGCTTCACAGGAAGTGGACCTATT 1379

274 HisLeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGl 290
        |||||||:||:|||:::|||
1380 CAGCTGTGGCAGTTTCCTCCGGAGCTGCTATCAGACAAAATCCTGC...CA 1426

290 uGlyLeuMetLysTrpGluAsnArgHisGluGly...ValPheLysPheL 306
        ::|||:|||:|||
1427 GTCATTCATCAGCTGGACTGGA.........GACCGGATGGGAGTTTAAGCTCG 1470

306 euArgSerGluAlaValAlaAlaGlnLeuTrpProGlyGlnLysLysAsnSer 322
        ::|:
1471 CCGACCCGATGAGGTGGCCCCCCGGTGGGGAAAGAGGAAAAAAATAAGCCC 1520

323 AsnMetThrTyrGluLysLeuSerArgAlaMetArgThrTyrTyrTyrLysAr 339
        ::|||||||||||:||:||||||||:||
1521 AAGATGAACTACGAGAAGCTGAGCCGGGCCTTACGCTTACTATTACGACA 1570

339 gGluIleLeuGluArgValAlaSpGlyArgArgLeuValTyrTyrLysPheGly 355
        ::|||:||||||||
1571 GAACATCATCCACAAGACGTCGGGAAGCGCTACGTGTTCACCTTCGTGT 1620

356 .........LysAsnSerGlyTrpLysGluGluGluVal 366
        :||:||
1621 GCGGACCTCCAGAACTTCGCTGGGGGTTCACGCCCGAGGAACTG 1661
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seq_name: /cgn2_6/ptodata/2/11a/5A_COMB.seq:US-08-306-691B-43

alignment_block:
US-08-978-217-2 x US-08-306-691B-43
US-08-306-691B-43

alignment_scores:
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          Quality:  228.00          Length:      435
          Ratio:    1.060           Gaps:         20
Percent Similarity: 49.425    Percent Identity: 23.218
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Align seq 1/1 to: US-08-306-691B-43 from: 1 to: 1604

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18 MetTyrSerSerGluAspSerThrLeuAlaSerValProProAlaAlaTh 34
      :::||:|||::::
345 CTTTTCCCCTCCCCCGGATATGGAAATGTGCAGAATGTCCCA.......... 383

34 rPheGlyAlaAspAspLeuValLeuThrLeuSerAsnProGlnMetSerL 51
      ::|||||||||:|::|
384 .........CTATTAACTCCAAGCAGCAAAGAAATGATGT 414

51 euGluGlyGly.................ThrGluLysAlaSerTrp 59
      |||:::|||
415 CTCAAGCATTAAAAAACTACTTTCAGTGGTTTCACTAAAGAACAACCAACGA 464

60 LeuGly.........GluGlnProGlnPheTrpProSerLysThrGlnValLeuAs 74
      ||||||          |||||:::||||||:
465 CTGGGGATCCCAAAAGACCCCCGGCAGTGGACAGAAAACCCATGTTCGGGA 514

74 pTrpIleSerTyrGlnValGlyLysAsnAspTyrAspAlaSerAlaIleaA 91
      |||||||||                ::||:::||||||
515 CTGGGTGATGTGGGCGTGTG.....AATGAATTCAGCCTGAAAGGTGTAG 558

91 spPheSerArgCysAspSerMetAspGlyAlaThrLeuCys 103
      |||||:::||:|:||                  ||:::||
559 ACTTCCAGAAGTTCTGTATGAATGGAGCAGCCCTCTGCGCCCTGGGTAAA 608

104 AsnCysAlaLeuGluGlnLeuArgLeuValPheGlyProLeuGlyAspGl 120
       ::||::||||:|||                :::|||||||
609 GACTGCTTTCTGCAG.................CTGGCCCCAGACTTTGGGGACAT 649

120 nLeuHisAlaGlnLeuArgAspLeu.................... 128
       |||                       :|:::::
650 CTTATGGGAACATCTAGACATCCTGCAGAAAGAGGATGTGAAACCATATC 699

129 .........ThrSerSerSerAspGluLeuSerTrpIleIleGlu 141
               |||                     :|:::
700 AAGTTAATGGAGTCAACCCAGCCTATCCAGAATCCCGGCTATACCTCGGAT 749

142 LeuLeuGlyLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPr 158
       |||||::|||||::|||                  |||
750 TACTTCATTAGCTATATGGTATTGAGCCATGCCCAGTGTTGTTCCACCATCGGA 799

158 oPheAspGlnGlySer.................... Prop 165
       ||||:|||                            |||
800 GTTCTGCAGACCCACCTTCATCACAGAGTCCTATCAGACAGCTTCCATCCCA 849

165 heAlaGlnGlu.................... 168
       |||
850 TCAGCTCCGGAAGAGCTCCTTCCCTCAAGTATGAGAATGACTACCCCCTCG 899

169 .........LeuLeuAspAspGlyGlnGlnAlaSerProTyrHis.......... 180
               ::|||                        ::|
900 GTCATTCTCCGAGACCCTCTCCAGACAGACACACCTTGCAGAATGACTACTT 949
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;
;   seq_documentation_block:
;   Sequence 9, Application PC/TUS9306251
;   GENERAL INFORMATION:
;   APPLICANT:
;     APPLICANT: Wickstrom, Eric and Rife, Jason P.
;   TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
;   TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
;   NUMBER OF SEQUENCES: 93
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
;     STREET: 400 Garden City Plaza
;     CITY: Garden City
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 11530
;   COMPUTER READABLE FORM:
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;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/06251
;   FILING DATE: 19930630
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: DiGiglio, Frank S.
;   REGISTRATION NUMBER: 31,346
;   REFERENCE/DOCKET NUMBER: 8586
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 516-742-4343
;   TELEFAX: 516-742-4366
;   TELEX: 230 901 SANS UR
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1604 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;   PCT-US93-06251-9
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alignment_scores:
    Quality:             228.00        Length:       435
    Ratio:                 1.060        Gaps:          20
Percent Similarity:       49.425    Percent Identity:  23.218

alignment_block:
US-08-978-217-2 x PCT-US93-06251-9

Align seq 1/1   to: PCT-US93-06251-9   from: 1   to: 1604
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```
181  ..........................ProGlySerCysGlyAlaGlyAlaP  189
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950  TGCTATCAAACAAGAAGTCGTCACCCCAGACACAGTGCATGGGGAGGA  999
     :||:|||

189  roSerProGly...........................SerSerAspValSer  197
     |||||:...|||
1000 CCAGTCGTGGTAAACTGGGGGGCCAGGACTCTTTTGAAAGCATAGAGAGC  1049

198  ThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGl  214
     :::|||
1050 TACGATAGTTGTGATCGCCTCACCCAGTCCATCTT  1099

214  ySerAspValAspLeuAspProThrAspGlyLysLeuPheProSerAspG  231
     :||:||
1100 CAACAGCCTGCAGCGTGTTCCCTCC...........TATGACAGCTTCG  1137

231  lyPheArgAspCysLysLysGlyAspProLysHisGlyLysArgLysArg  247
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1138 ACTCAGAGACACTATCCGGCTGCCCTGCCCCAACCAC  1172

248  GlyArgProArgGlyLeuSerLysGluTyr...TrpAspCysLeuGluGl  263
     ::||:|||
1173 ..AAGCCCAAGGGACACCTTCAAGGACTATGTCGGGACACCGTGCTGACCT  1219

263  yLysLysSerLys......................HisAlaP  270
     ::|::|||
1220 CAATAAGGACAAGCCTGTCATTCCTGCTGCCTAGCTGGCTACACAG  1269

270  roArgGly...ThrHisLeuTrpGluPheIleArgAspIleLeuIleHis  285
     |||:|||::|||
1270 GCAGTGGACCAATCCAGCTATGCAGTTTCTTCTGGAATTACTCACTGAT  1319

286  ProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly..  301
     ::|||
1320 AAATCCTGT...CAGTCTTTATCAGCTGGGACAGA.....GATGGCTG  1360

302  .ValPheLysPheLeuArgSerGluAlaValAlaLAlaGInLeuTrpGlyGInL  318
     |||||||::|||
1361 GGAATTCAAACTTTCTGACCCAGATGAGGTGGGCCAGGATGGGGAAAGA  1410

318  ySLysLysLysAsnSerAsnMetThrTyrGluLysSerArgAlaMetArg  334
     ::|||||||||||||||
1411 GGAAAACAAAACCTAAGATGAATTATGAGAAACTGAGCCGTGCCCTACGC  1460

335  TyrTyrTyrLysArgGluIleLeuGluIleArgValAspGlyArgArgLeuVa  351
     ||||||||||||||                    ThrGluLysAlaSerTrp  59
1461 TACTATTTACGACAAAAACATCCACAAGACAGCGGGGAAACGGCTACGT  1510

351  lTyrLysPheGly...........LysAsnSerSerGlyTyrTrpLysGluGlu  365
     |||||||||||                         |||||
1511 GTACCGCTTTGTGTGTGACCTGCAGAGCCCTGCTGGGGTACACCCCTGAGG  1560

365  luVal  366
     ||:::|
1561 AGCTG  1565
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```
18   MetTyrSerSerGluAspSerThrLeuAlaSerValProProAlaAlaTh  34
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34   rPheGlyAlaAspAspLeuValLeuThrLeuSerAsnProGlnMetSerL  51
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384  ...............CTATTAACTCCAAGCACCAGCAAAGAAAATGATGT  414

51   euGluGly........................ThrGluLysAlaSerTrp  59
     :::||||                                    :||||:|
415  CTCAAGCATTAAAAACCTACTTTCAGTGGTTTCACTAAGAACAGCAACGA  464

60   LeuGly...........GluGlnProGlnPheThrpSerLysThrGlnValLeuAs  74
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465  CTGGGGATCCCAAAAAGACCCCCGGCAGTGGACAGAAACCCATGTTCGGGA  514

74   pTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIleA  91
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515  CTGGGGTGGATGTGGGCTGTG........AATGAATTCAGCCTGAAAAGGTGTAG  558

91   spPheSerArgCysAspMetAspGlyAlaThrLeuCys...........  103
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559  ACTTCCAGAAGTTCTGTATGAATGGAGCAGCCCTCTGCGCCCTGGGTAAA  608

104  AsnCysAlaIleGluGluLeuGluValPheGlyProLeuGlyAspGl  120
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609  GACTCGCTTCTCCGAG..............CTGGCCCCAGACTTTGTTGGGGACAT  649

120  nLeuHisSerLeuGlnLeuArgAspLeu...................  128
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650  CTTTATGGGAACACTCTAGAGARCCTCCAGAAAGAGGATGTGAAAACCATATC  699

129  ..........ThrSerSerSerAspSerGluLeuSerTrpIleIleGlu  141
     ::|||                    :||
700  AAGTTAATGGAGTCAACCCAGCCTATCCAGAATCCCGGCTATACCTACGGAT  749

142  LeuLeuGluLysAspGlyMetAlaPheGlnGluLeuAlaLeuAspProGlyPr  158
```

```
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 158 opheAspGlnGlySer.......................ProP 165
 800 GTTCTCAGAGCCCAGCTTCATCACAGAGTCCTATCAGAGACGTCCATCCCA 849
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 165 heAlaGlnGlu.......................... 168
 850 TCAGCTCGGAAGAGCTCCTCTCCCTCAAGTATGAGAATGACTACCCCTCG 899
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 169 ..LeuLeuAspAspGlyGlnGlnAlaSerProTyrHis......... 180
 900 GTCATTCCTCCGAGACCCTCTCCAGACAGCACCTTCGAGAATGACTACTT 949
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 181 ......ProGlySerCysGlyAlaGlyAlaP 189
 950 TGCTATCAAACAAGAGAAGTGTCACCCCAGACAACACATGTCATGGGGAGGA 999
     |||  |::                              |||
 189 roSerProGly...................SerSerAspValSer 197
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 198 ThrAlaGlyThrGlyAlaSerArgSerHisSerSerAspSerGlyGl 214
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 214 ySerAspValAspLeuAspProThrAspPGlyLysLeuPheProSerAspG 231
1100 CAACAGCCCTGCGACGCGTGTTCCCTCC........TATGACAGCTTCG 1137
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 231 lyPheArgAspCysGlySerGlyAspProLysHisGlyLysArgLysArg 247
1138 ACTCAGAGGACTATCCGGCTGCCCTGCCCAACCAC.......... 1172
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 248 GlyArgProArgLysLeuSerLysGluTyr...TrpAspCysLeuGluGl 263
1173 ..AAGCCCAAGGGCACCTTCAAGGACTATGTGCGGGACAGCGTGCTGACCT 1219
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 263 yLysLysSerLys...................HisAlaP 270
1220 CAATAAGGACAAAGCCTGTCATTCCTCCTGCTGCCCCTAGCCTGCTACACAG 1269
     :::|||::|||
 270 roArgGly...ThrHisLeuTrpGluPheIleArgAspIleLeuIleHis 285
1270 GCAGTGGACCAATCCAGCTATGGCAGTTTCTTCTGGAATTACTCACTGAT 1319
     :::|||||:::|||
 286 ProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
1320 AAATCCTGT....CAGTCTTTTATCAGCTGGACAGGA.....GATGGCTG 1360
     |||||                      |||||
 302 .ValPheLysPheLeuArgSerGluAlaValAlaGlnIleLeuTrpGlyGln 318
1361 GGAATTCAAACTTTCTGACCCAGATGAGGTGGCCAGAGATGGGGAAAGA 1410
     |||||::                      |||||
 318 ysLysLysAsnSerAsnMetThrTyrGluLeuSerArgAlaMetArg 334
1411 GGAAAAACAAACCTAAGATGAATTATGAGAAACTGACCGTGGCCTACGC 1460
     |||::||||||||||||||||:::::|||
 335 TyrTyrTyrPheLysArgGluIleLeuArgValAspGlyArgArgLeuVa 351
1461 TACTATTACGACAAAAACATCACAAGACAGAGGCAGAGGCTAGT 1510
     ||||||||||||||||
 351 lTyrLysPheGlu.........LysAsnSerGlyTyrPheLysGluLuG 365
1511 GTACCGCCTTGTGTGTGACCTGCAGAGGCCTGCTGGGGTACACCCCTGAGG 1560
     |||||||:|||                          ||||
 365 luVal 366
1561 AGCTG 1565
```

```
alignment_scores:
            Quality: 212.00                    Length:  328
              Ratio:   1.395                     Gaps:   12
 Percent Similarity: 46.341     Percent Identity: 23.171

alignment_block:
 US-08-978-217-2 x US-08-343-443B-3

Align seq 1/1   to: US-08-343-443B-3   from: 1   to: 2938

  47 ProGlnMetSerLeuGlyGlyThrGluLysAlaSerTrpLeuGlyGluGl 63
     |||       ::::::: | :::|||
 479 CCTCCTCCCAACATGACCAACGAGGACCAACGAGGAGGAGTCATCGTCCCGCAGA 528
```

```
 63 nProGlnPheTrpSerLysThrGlnValLeuAspThrTrpIleSerTyrGlnV  80
    |||        :|||||||||||||      :||||     |||:||||||||||:
529 CCCCACACTGTGGACACAGGAGCATGTGAGCCAATGGCTGGAGTGGGGCCA   578

 80 alGluLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCys...    95
    :::||||||||     |||||      |||||||||||       |||
579 TAAAG........GAGTATAGCTTGATGGAGGATCGACACATCCTTTTTCCAG  622

 96 AspMetAspGlyAlaThrLeuCysLysAsnCysAlaLeuGluGluArgIle   112
    ||||||||||||||     |||      :::         ::||||
623 AACATGGATGGCAAGGAACTGTGTAAAATGAACAAGGAGACTTC.....    667

112 uValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuT   129
    |||||||                |                   |||||
668 ..............................CTCCGCGCCACCA          680

129 hrSerSerSerSerAspGlu...LeuSerTrpIleIleGluLeuLeuGlu   144
    ||:::::::::||||||||||||||                |:        ||
681 CCCTCTACAACACGGAAGTGCTGTTGTCACACCTCAGTTACCTCAGGGAA   730

145 LysAspGlyMetAlaPheGlnGluAlaLeuGluAspProGlyProPheAspGl   161
    ::::|||||||||||      ||||                   |||
731 AGTTCACTGCTGGCCTAT.................................  748

161 nGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerP   178
    ...................................              748

178 roTyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSer   194
    ::::::::::::::::::::         AATACAACCTCCCACCGACCA  748

195 AspValSerThrAlaGlyThrGlyAlaSerArgSerHisSerSerAs    211
    :::         AATACAACCTCCCACCGACCA                771

211 pSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe   228
    ::|      |:|||||||||||||||:::::
772 ATCCTCACGATTGAGTGTCAAAAGAAGAACCCTTCT.............  805

228 roSerAspGlyPheArg.................              Asp  234
    ||||
806 .TATGACTCAGTCAGAAGAGGAGCATGGGGCGCAATAACATGAATTCTGGC  853

235 CysLysLysGlyAspHisGly...............    LysArgGly   246
    ::|||:||                           |||
854 CTCAACAAAAGTCCTCCCCTTGGAGGGGCACAAACGATCAGTAAGAATAC  903

246 sArgGlyArgProArgLysLysSerGlyTyrTrpAspCysLeuGluG    263
    |||||||||||||::||
904 AGAGCAACGGCCCCAG..........CCAGATCCGTATCAGATCCTGGGCC  944

263 lyLysLysSerLysHisAlaProArgGlyThr........HisLeuTrp  276
    :::|||:         :::||||||||
945 CGACCAGCAGTCGCCTAGCCAACCCTGGAAGCGGGGCAGAATCCAGCTGTGG  994

277 GluPheIleArgAspIleLeuHisProGluLeuAsnGluGlyLeuMe    293
    ::|||||       |||:::
995 CAATTCCTCCTGGAG...CTGCTCTCCGACAGCGCCAACGCCAGCTGTAT  1041

293 tLysTrpGluAsnArgHisGlyGlyValPheLysPheLeuArgSerGluA    310
    :|||||:         |||
1042 CACCTGGGAGGGGACCAAC..GGGGAGTTCAAAATGACGGACCCCCGATG  1088

310 laValAlaGluGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetThrTyr  326
    ||||||||||||||||::||::::::::       ||||||||::::||||
1089 AGGTGGCCGAGCGCGCTGGGGCAGAAGGGAAAAAAGCCCAACATGAAATTAC 1138

327 GluLysLeuSerArgAlaAlaMetArgThrTyrTyrLysArgGluIleLeuGl  343
    ::|||||||||||||||||||::|:::|||||||||||||:||||:::||||
1139 GACAAGCTGACCCGGACCCGGGCCCTCCGTTATTACTATAAAAAACATTATGAC 1188

343 uArgValAspGlyArgLeuValTyrLysPhe 354
```